

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/089,211B
Source: IFW/6
Date Processed by STIC: 11/9/04

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/089,211B

DATE: 11/09/2004

TIME: 12:46:43

Input Set : A:\62447-01.ST25.txt

Output Set: N:\CRF4\11092004\J089211B.raw

Q6

3 <110> APPLICANT: University of Victoria Innovation and Developement
 4 Corporation
 5 Hintz, William E.
 6 Eades, Caleb Joshua
 8 <120> TITLE OF INVENTION: Mannosidases and Methods for using the Same
 10 <130> FILE REFERENCE: 2847-62447-01
 12 <140> CURRENT APPLICATION NUMBER: 10/089,211B
 13 <141> CURRENT FILING DATE: 2002-03-25
 15 <150> PRIOR APPLICATION NUMBER: PCT/US00/27210
 16 <151> PRIOR FILING DATE: 2000-10-02
 18 <150> PRIOR APPLICATION NUMBER: 60/157,341
 19 <151> PRIOR FILING DATE: 1999-10-01
 21 <160> NUMBER OF SEQ ID NOS: 19
 23 <170> SOFTWARE: PatentIn version 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 3328
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Aspergillus nidulans
 30 <400> SEQUENCE: 1

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| 33 | taatttctggg gaccgatatac ccttgaacgc gggggcaatc agttcaacca accccagacccg | 120 |
| 35 | ctgggcttgg tatgagattt cgagccatcta tgcgtgttgc ccttctgaat gacaatgaat | 180 |
| 37 | gtattttact tctcgaaaaag aacccttggg cactgaatttgc tgccggagaat gatgccctga | 240 |
| 39 | ttatgataca actagtccgc tccgtcaagc cacaagggtc tgggcagtcc gctataaattc | 300 |
| 41 | aaaatcgccct gcacgaacag acgaataacc aagaaaaacgc ccgagcgcga gcgtttcttc | 360 |
| 43 | tccctctaag cttgcagct ggctctgcgt ctgtatcaa cccttttagct gaatttcccc | 420 |
| 45 | agaacttcag ccctctgcgt cctgtcctta ccgcactcg ttaacctgcg cgacctcgcg | 480 |
| 47 | cgaccacagc ctttagtttc gagatgccat gaaaatcaga aattgaaccc cttttccatt | 540 |
| 49 | actatcattc tctgcatttc gcgagtgtatc tgcgttgcg cgttccctt ttccagcgct | 600 |
| 51 | gcgggcctt cactctcggt gcctacgtt gaccacggtc ctacctctcc tactgctgtat | 660 |
| 53 | tatttaggcgc ctccctacgc ctccaaataca gggaaatgcg cggccatgtt tgcgtacgca | 720 |
| 55 | cgatctcgca tctcgctggt gtttgcgtt atatttgcgc tcctcatatt ccactttacgc | 780 |
| 57 | cgtctcgcaatcg ttacgatcag cctgcaatct tgggtacactc cgccgcggcgt cgatcaccat | 840 |
| 59 | aatccccctt tccccgacca gaacctcaaa gatccatacg aaaacgacaa tagtgcgacc | 900 |
| 61 | ggcagtgggg ctccctccgc tgcgttggta gagccagaag aataccaacg accaccactt | 960 |
| 63 | tacacagatt cagatgacag cccaaactccg tcaaaagaac gcctggacac cccgagcaat | 1020 |
| 65 | gtcccatctc aggagcctga atttgcgttgc gcccggactt agacgggtgc gcagacccaa | 1080 |
| 67 | aataaaatcg aagatgtatc ggtatattgtc ccaatttctc actggaaatcg gatgcccgaa | 1140 |
| 69 | cgccatccag tcagtcggaa ggctttgtatc aagctgcacca ccgggcaatc aaaggaactc | 1200 |
| 71 | ccccaaactgc aagctaagtt caaggacgag tcgttgcgttgc acaagatgc gcccgtgca | 1260 |
| 73 | caacttgaca ctatcaagtc ggcgttctta catgcgttgc acggttacaa gatctctgc | 1320 |
| 75 | atgggtcatg atgaggttag acctctgcgc ggtggttca aggacacatt caatggctgg | 1380 |
| 77 | ggcgcgaccc ttgtcgacgc ctggatacc ctgtggatca tggatctcaa agaggagttc | 1440 |

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| 79 | tccatggcag | tcgactacgt | caagaaaatc | gattttacca | ccagcaccaa | gaaaagagatt | 1500 |
| 81 | ccggctttg | aaaccactat | tcgctaccta | ggcgggatgc | tcggggccta | tgatatttcg | 1560 |
| 83 | ggacacaaat | acgatatact | tttggaaaag | tctgttgagc | ttgcggatgt | cttgatggac | 1620 |
| 85 | gccttcgaca | caccgaaccg | gatccaaacc | ctctattata | aatggagccc | agagtatgct | 1680 |
| 87 | tcagagttc | gccgggggga | ctttaaggct | gttctcgccg | agcttggctc | tctctcttc | 1740 |
| 89 | gagttcacgc | gttggcgca | gttgacccaa | caggacaagt | actacatgc | aattgcacga | 1800 |
| 91 | atcacaaatg | agctcgaaaa | gtatcaggat | ttgacaaaagc | ttcccgctt | gtggcctctc | 1860 |
| 93 | aacctggacg | catccgggt | caggcgagtt | ccggcgctc | cgcgagagcc | tgctgcgct | 1920 |
| 95 | gggcagccag | ttagatggtc | ctctgacgag | atcaactcga | cgagctcggt | atcgatcg | 1980 |
| 97 | acaagacaaa | ttcatgaggg | cgagagccct | gtccgtcatg | acaatgattc | gtttgaaacg | 2040 |
| 99 | gttttcctg | tatcagtcta | tactcggact | cctcccccac | agcaagattg | caccggaggc | 2100 |
| 101 | ctcaacgatc | agctctcagg | cattgacaaag | ttcggactcg | gagcccttgg | tgactctacg | 2160 |
| 103 | tacgagtact | taccgaaaga | gtatatgtt | ctcggcggt | acaacgacca | gtacctaacc | 2220 |
| 105 | atgtatcaga | aggccatgg | cacagtgcga | gaatatctt | tttatcagcc | aatgctcaag | 2280 |
| 107 | aataatcgcg | atgtccgctt | cttagcaca | gttagtatga | caaagagcct | tgatgcaaac | 2340 |
| 109 | cctccggggc | gtaccactt | cgcgtacgaa | ggcactcacc | tcacctgtt | tgctgggt | 2400 |
| 111 | atqcttgc | ttggcgccaa | gttgggg | cttgataagg | atctaaagct | gggtagtcaa | 2460 |
| 113 | ctgacggacg | gctgtgtctg | ggcatatgaa | gccacaaagt | ccggaatcat | gccggaaagca | 2520 |
| 115 | ttccaactgg | tccctgttaa | gaaaggcgag | ccatgcgaat | gggatgagga | cgcataactac | 2580 |
| 117 | atgccccatgg | atccttatgc | cgacaagcg | ccaatatcac | ataacaaacg | ctccgcggc | 2640 |
| 119 | cctgaaaagg | ggaattggca | cgtcgccg | acagccgaat | cgtttcgcc | ccaggaagat | 2700 |
| 121 | aaaacacaga | aatcaaccac | tactgagggt | cgacacaccg | gtacaactac | cggggcaggc | 2760 |
| 123 | gcgcctcgc | acgaggaatt | cgtcacggg | aaaatcctca | acgaccgact | ccgcggggc | 2820 |
| 125 | atgacaggga | tctcggtctg | gcagtacctc | cttcgcccgg | aggcgatcga | gtctgtctc | 2880 |
| 127 | atcatgttcc | gcctcacggg | cgatccttcc | tggcgaaaa | agggttgaa | gatgttccag | 2940 |
| 129 | gctgtcgaca | aagccacgaa | gacggagctg | gcgaactcgg | ccatttccga | cgttaaccgtc | 3000 |
| 131 | gataatccac | gccccgggt | cagtatggaa | tcattctggc | ttgcggagac | tctgaaatac | 3060 |
| 133 | ttctacctt | ttttcagcga | tccaaagcctg | gtgagcctt | acgaatatgt | cttgtaaatg | 3120 |
| 135 | atgttgcact | taatcgact | tttgatgctg | actttccct | taggaacacc | gaggctcatc | 3180 |
| 137 | cgttcaagcg | acccaagtagc | tgaagtagta | atttaaatga | tcttttagcc | tgtatctata | 3240 |
| 139 | catggccgct | ccgctgtaga | agcattgata | ccattaagac | agtatcgctg | cattcgtgt | 3300 |
| 141 | ccatggc | ttccagagga | acctctt | | | | 3328 |
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| 145 | <211> | LENGTH: | 2448 | | | | |
| 146 | <212> | TYPE: | DNA | | | | |
| 147 | <213> | ORGANISM: | Aspergillus nidulans | | | | |
| 150 | <220> | FEATURE: | | | | | |
| 151 | <221> | NAME/KEY: | misc_feature | | | | |
| 152 | <222> | LOCATION: | (1632)..(1632) | | | | |
| 153 | <223> | OTHER INFORMATION: | n is a, g, c, or t/u | | | | |
| 155 | <400> | SEQUENCE: | 2 | | | | |
| 156 | atgttgcgt | cacgacgatc | tcgcacatctcg | ctgggttttgc | ccgttatatt | tgtcctcttc | 60 |
| 158 | atattccact | ttagccgtct | cgcagttacg | atcagcctgc | aatcttgggt | accccgccg | 120 |
| 160 | cccgctgatc | accataatcc | ccctttcccc | gaccagaacc | tcaaagatcc | atacgaaaac | 180 |
| 162 | gacaatagtg | cgaccggcag | tggggctt | ccgcctcggt | tgttagagcc | agaagaatac | 240 |
| 164 | caacgaccac | cactttacac | agattcagat | gacagccaa | ctccgtcaaa | agaacgcctg | 300 |
| 166 | gacaccccgaa | gcaatgtccc | atctcaggag | cctgaatttgc | atgcccggcag | acttcagacg | 360 |
| 168 | ggtgcgcaga | cccaaaataa | acatgaagat | gatgaggata | ttgtcccaat | ttctcactgg | 420 |
| 170 | aagccgatgc | ccgaacggca | tccagtcgt | ccggaggctt | tgtcaagct | gccaaccggg | 480 |

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|----------|-------------|-------------|--------------|--------------|-------------|-------------|------|
| 172 | caatcaaagg | aactccccc | actgcaagct | aagttcaagg | acgagtcgtc | ctcgacaaag | 540 |
| 174 | atgcagcggc | tgcaacaact | tgacactatc | aagtccggct | tcttacatgc | gtggaaacgg | 600 |
| 176 | tacaagatct | ctgcccattgg | tcatgatgag | gttagaccc | tgcgcgtgg | tttcaaggac | 660 |
| 178 | acattcaatg | gctggggcgc | gacccttgc | gacgccttgg | ataccctgtg | gatcatggat | 720 |
| 180 | ctcaaaagagg | agttctccat | ggcagtcac | tacgtcaaga | aaatcgatt | taccaccagc | 780 |
| 182 | accaagaaag | agattccgg | ctttgaaacc | actattcgct | acctaggcgg | gtatgcgtgg | 840 |
| 184 | gcctatgata | tttcgggaca | caaatacgt | atacttttg | aaaagtctgt | tgagcttgcg | 900 |
| 186 | gatgtcttga | tggacgcctt | cgacacaccg | aaccggatgc | caaccctcta | ttataaaatgg | 960 |
| 188 | agccagagt | atgcttcaga | gttgcggg | ggggactta | aggctgttct | cggcggagctt | 1020 |
| 190 | ggctctctct | ctctcgagtt | cacgcgttgc | gcccgcgttgc | ccaaacacgg | caagtaactac | 1080 |
| 192 | gatcaatttgc | cacgaatcac | aaatgagctc | gaaaagtatc | aggatttgac | aaagcttccc | 1140 |
| 194 | ggcttgcgtgc | ctctcaacct | ggacgcaccc | gggtgcaggc | gagttcccg | cgtctcgca | 1200 |
| 196 | gagcctgcgt | cggctggca | gccagtcaga | tggtcctctg | acgagatcaa | ctcgacgagc | 1260 |
| 198 | tcggatcgat | atcgatcaag | acaaattcat | gagggcggag | agctgtccg | tcatgacaat | 1320 |
| 200 | gattcgtttgc | aaacgggttgc | tcctgtatca | gtcgataactc | ggactctcc | cccaaagcaa | 1380 |
| 202 | gattgcaccc | gaggcctcaa | cgatcagctc | tcaggcatttgc | acaagttcg | actcggagcc | 1440 |
| 204 | cttgggtact | ctacgtacga | gtacttaccg | aaagagtata | tgttgctcg | cggttaacaac | 1500 |
| 206 | gaccagtacc | tcaacatgt | tcagaaggcc | atggacacag | tgcgagaata | tcttggttat | 1560 |
| 208 | cagccaatgc | tcaagaataa | tcgcgtatgc | cgcttcttag | cgacagtttgc | tatgacaaag | 1620 |
| W--> 210 | agccttgcgt | cnaaaccc | ggggcgtacc | actttcgct | acgaaggcac | tcacccatc | 1680 |
| 212 | tgtttgcgt | gtggatgt | tgccattggc | gccaagtgt | ttgggcttgc | taaggatcta | 1740 |
| 214 | aagctggta | gtcaactgac | ggacggctgt | gtctggcat | atgaagccac | aaagtcgg | 1800 |
| 216 | atcatgcgg | aagcattcca | actggcccttgc | tgtaagaaag | gcgagccatg | cgaatggat | 1860 |
| 218 | gaggacgcac | actacatggc | catggatcttgc | tatgccgaca | agcggccat | atcacataac | 1920 |
| 220 | aaacgctccg | ccggccctga | aaagggaaat | tggcacgtc | tcggccacagc | cgaatcgct | 1980 |
| 222 | tcgccccagg | aagataaaac | acagaaatca | accactactg | agggtcgaca | caccggata | 2040 |
| 224 | actaccgggg | caggcgcgt | ctcgacacgg | gaattcgta | cggaaaaat | cctcaacgc | 2100 |
| 226 | cgactcccgc | cgggcgtac | aggatctcg | gctcgccagt | accccttc | cccgaggcg | 2160 |
| 228 | atcgagtctg | tcttcatcat | gttccgcctc | acgggcgtc | cttccctggcg | cgaaaagggt | 2220 |
| 230 | tggaaagatgt | tccaggctgt | cgacaaagcc | acgaagacgg | agctggcgaa | ctcgccatt | 2280 |
| 232 | tccgacgtaa | ccgtcgat | tccacgc | gtggacagta | tggaaatcatt | ctggcttgc | 2340 |
| 234 | gagactctg | aataacttcta | ccttcttttc | agcgatccaa | gcctgggtg | cttgaggaa | 2400 |
| 236 | tatgtcttgc | acaccggggc | tcatccgttgc | aagcgaccc | ggtactga | | 2448 |

239 <210> SEQ ID NO: 3

240 <211> LENGTH: 815

241 <212> TYPE: PRT

242 <213> ORGANISM: Aspergillus nidulans

244 <400> SEQUENCE: 3

246 Met Phe Arg Ala Arg Arg Ser Arg Ile Ser Leu Val Phe Ala Val Ile

247 1 5 10 15

250 Phe Val Leu Leu Ile Phe His Phe Ser Arg Leu Ala Val Thr Ile Ser

251 20 25 30

254 Leu Gln Ser Trp Val Pro Pro Pro Val Asp His His Asn Pro Pro

255 35 40 45

258 Phe Pro Asp Gln Asn Leu Lys Asp Pro Thr Glu Asn Asp Asn Ser Ala

259 50 55 60

262 Thr Gly Ser Gly Ala Pro Pro Ala Leu Val Glu Pro Glu Glu Thr

263 65 70 75 80

266 Gln Arg Pro Pro Leu Thr Thr Asp Ser Asp Asp Ser Pro Thr Pro Ser

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|-----|---|-----|-----|-----|
| 267 | 85 | 90 | 95 | |
| 270 | Lys Glu Arg Leu Asp Thr Pro Ser Asn Val Pro Ser Gln Glu Pro Glu | | | |
| 271 | 100 | 105 | 110 | |
| 274 | Phe Asp Ala Ala Arg Leu Gln Thr Gly Ala Gln Thr Gln Asn Lys His | | | |
| 275 | 115 | 120 | 125 | |
| 278 | Glu Asp Asp Glu Asp Ile Val Pro Ile Ser His Trp Lys Pro Met Pro | | | |
| 279 | 130 | 135 | 140 | |
| 282 | Glu Arg His Pro Val Ser Pro Glu Ala Leu Ile Lys Leu Pro Thr Gly | | | |
| 283 | 145 | 150 | 155 | 160 |
| 286 | Gln Ser Lys Glu Leu Pro Gln Leu Gln Ala Lys Phe Lys Asp Glu Ser | | | |
| 287 | 165 | 170 | 175 | |
| 290 | Ser Ser Asp Lys Met Gln Arg Leu Gln Gln Leu Asp Thr Ile Lys Ser | | | |
| 291 | 180 | 185 | 190 | |
| 294 | Ala Phe Leu His Ala Trp Asn Gly Thr Lys Ile Ser Ala Met Gly His | | | |
| 295 | 195 | 200 | 205 | |
| 298 | Asp Glu Val Arg Pro Leu Arg Gly Gly Phe Lys Asp Thr Phe Asn Gly | | | |
| 299 | 210 | 215 | 220 | |
| 302 | Trp Gly Ala Thr Leu Val Asp Ala Leu Asp Thr Leu Trp Ile Met Asp | | | |
| 303 | 225 | 230 | 235 | 240 |
| 306 | Leu Lys Glu Glu Phe Ser Met Ala Val Asp Thr Val Lys Lys Ile Asp | | | |
| 307 | 245 | 250 | 255 | |
| 310 | Phe Thr Thr Ser Thr Lys Lys Glu Ile Pro Val Phe Glu Thr Thr Ile | | | |
| 311 | 260 | 265 | 270 | |
| 314 | Arg Thr Leu Gly Gly Met Leu Gly Ala Thr Asp Ile Ser Gly His Lys | | | |
| 315 | 275 | 280 | 285 | |
| 318 | Thr Asp Ile Leu Leu Glu Lys Ser Val Glu Leu Ala Asp Val Leu Met | | | |
| 319 | 290 | 295 | 300 | |
| 322 | Asp Ala Phe Asp Thr Pro Asn Arg Met Pro Thr Leu Thr Thr Lys Trp | | | |
| 323 | 305 | 310 | 315 | 320 |
| 326 | Ser Pro Glu Thr Ala Ser Glu Phe Arg Arg Gly Asp Phe Lys Ala Val | | | |
| 327 | 325 | 330 | 335 | |
| 330 | Leu Ala Glu Leu Gly Ser Leu Ser Leu Glu Phe Thr Arg Leu Ala Gln | | | |
| 331 | 340 | 345 | 350 | |
| 334 | Leu Thr Lys Gln Asp Lys Thr Thr Asp Ala Ile Ala Arg Ile Thr Asn | | | |
| 335 | 355 | 360 | 365 | |
| 338 | Glu Leu Glu Lys Thr Gln Asp Leu Thr Lys Leu Pro Gly Leu Trp Pro | | | |
| 339 | 370 | 375 | 380 | |
| 342 | Leu Asn Leu Asp Ala Ser Gly Cys Arg Arg Val Pro Gly Val Ser Arg | | | |
| 343 | 385 | 390 | 395 | 400 |
| 346 | Glu Pro Ala Ala Ala Gly Gln Pro Val Arg Trp Ser Ser Asp Glu Ile | | | |
| 347 | 405 | 410 | 415 | |
| 350 | Asn Ser Thr Ser Ser Val Ser Thr Arg Thr Arg Gln Ile His Glu Gly | | | |
| 351 | 420 | 425 | 430 | |
| 354 | Gly Glu Pro Val Arg His Asp Asn Asp Ser Phe Glu Thr Gly Phe Pro | | | |
| 355 | 435 | 440 | 445 | |
| 358 | Val Ser Val Asp Thr Arg Thr Pro Pro Pro Lys Gln Asp Cys Thr Gly | | | |
| 359 | 450 | 455 | 460 | |
| 362 | Gly Leu Asn Asp Gln Leu Ser Gly Ile Asp Lys Phe Gly Leu Gly Ala | | | |
| 363 | 465 | 470 | 475 | 480 |

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366 Leu Gly Asp Ser Thr Thr Glu Thr Leu Pro Lys Glu Thr Met Leu Leu
 367 485 490 495
 370 Gly Gly Asn Asn Asp Gln Thr Leu Asn Met Thr Gln Lys Ala Met Asp
 371 500 505 510
 374 Thr Val Arg Glu Thr Leu Val Thr Gln Pro Met Leu Lys Asn Asn Arg
 375 515 520 525
 378 Asp Val Arg Phe Leu Ala Thr Val Ser Met Thr Lys Ser Leu Asp Ala
 379 530 535 540
 382 Asn Pro Pro Gly Arg Thr Thr Phe Ala Thr Glu Gly Thr His Leu Thr
 383 545 550 555 560
 386 Cys Phe Ala Gly Gly Met Leu Ala Ile Gly Ala Lys Leu Phe Gly Leu
 387 565 570 575
 390 Asp Lys Asp Leu Lys Leu Gly Ser Gln Leu Thr Asp Gly Cys Val Trp
 391 580 585 590
 394 Ala Thr Glu Ala Thr Lys Ser Gly Ile Met Pro Glu Ala Phe Gln Leu
 395 595 600 605
 398 Val Pro Cys Lys Lys Gly Glu Pro Cys Glu Trp Asp Glu Asp Ala Thr
 399 610 615 620
 402 Thr Met Ala Met Asp Pro Thr Ala Asp Lys Arg Pro Ile Ser His Asn
 403 625 630 635 640
 406 Lys Arg Ser Ala Gly Pro Glu Lys Gly Asn Trp His Val Val Ala Thr
 407 645 650 655
 410 Ala Glu Ser Ser Pro Gln Glu Asp Lys Thr Gln Lys Ser Thr Thr
 411 660 665 670
 414 Thr Glu Gly Arg His Thr Gly Thr Thr Gly Ala Gly Ala Leu Ser
 415 675 680 685
 418 His Glu Glu Phe Val Thr Gly Lys Ile Leu Asn Asp Arg Leu Pro Pro
 419 690 695 700
 422 Gly Met Thr Gly Ile Ser Ala Arg Gln Thr Leu Leu Arg Pro Glu Ala
 423 705 710 715 720
 426 Ile Glu Ser Val Phe Ile Met Phe Arg Leu Thr Gly Asp Pro Ser Trp
 427 725 730 735
 430 Arg Glu Lys Gly Trp Lys Met Phe Gln Ala Val Asp Lys Ala Thr Lys
 431 740 745 750
 434 Thr Glu Leu Ala Asn Ser Ala Ile Ser Asp Val Thr Val Asp Asn Pro
 435 755 760 765
 438 Arg Pro Val Asp Ser Met Glu Ser Phe Trp Leu Ala Glu Thr Leu Lys
 439 770 775 780
 442 Thr Phe Thr Leu Leu Phe Ser Asp Pro Ser Leu Val Ser Leu Glu Glu
 443 785 790 795 800
 446 Thr Val Leu Asn Thr Glu Ala His Pro Phe Lys Arg Pro Arg Thr
 447 805 810 815
 450 <210> SEQ ID NO: 4
 451 <211> LENGTH: 2177
 452 <212> TYPE: DNA
 453 <213> ORGANISM: Aspergillus nidulans
 455 <400> SEQUENCE: 4
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 458 ccatcatggg acggtccttg atcctcaagg cacgaagtgg agatcaggc cgtagtgc 120

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/09/2004
PATENT APPLICATION: US/10/089,211B TIME: 12:46:44

Input Set : A:\62447-01.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 1682
Seq#:8; N Pos. 4
Seq#:15; N Pos. 9,18
Seq#:16; N Pos. 4,13,16,22,25

VERIFICATION SUMMARY

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L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1620
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0